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1644

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/766,350A

DATE: 05/26/98
TIME: 09:45:47

INPUT SET: S26074.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#12/JR
08/26/98

1

SEQUENCE LISTING

2

3 (1) General Information:

4

5 (i) APPLICANT: Chatterjee, Malaya
6 Foon, Kenneth A.
7 Chatterjee, Sunil K.

8

9 (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
10 11D10 AND METHODS OF USE THEREOF

11

12 (iii) NUMBER OF SEQUENCES: 59

13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 PAGE MILL ROAD
17 (C) CITY: PALO ALTO
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018

21

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US 08/766,350
30 (B) FILING DATE: 13-DEC-1996
31 (C) CLASSIFICATION:

32

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Polizzi, Catherine M.
35 (B) REGISTRATION NUMBER: 40,130
36 (C) REFERENCE/DOCKET NUMBER: 30414-20003.21

37

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: (650) 813-5600
40 (B) TELEFAX: (650) 494-0792
41 (C) TELEX: 706141

42

43

44 (2) INFORMATION FOR SEQ ID NO:1:

45

46 (i) SEQUENCE CHARACTERISTICS:

ENTERED

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47 (A) LENGTH: 435 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: DNA (genomic)
53
54
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..435
58
59 (ix) FEATURE:
60 (A) NAME/KEY: mat_peptide
61 (B) LOCATION: 61
62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48
67 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
68 -20 -15 -10 -5
69
70 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96
71 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
72 1 5 10
73
74 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144
75 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
76 15 20 25
77
78 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192
79 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
80 30 35 40
81
82 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240
83 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
84 45 50 55 60
85
86 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288
87 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
88 65 70 75
89
90 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336
91 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
92 80 85 90
93
94 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384
95 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
96 95 100 105
97
98 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432
99 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu

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100 110 115 120 435
 101
 102 GGG
 103 Gly
 104 125
 105
 106
 107 (2) INFORMATION FOR SEQ ID NO:2:
 108
 109 (i) SEQUENCE CHARACTERISTICS:
 110 (A) LENGTH: 145 amino acids
 111 (B) TYPE: amino acid
 112 (D) TOPOLOGY: linear
 113
 114 (ii) MOLECULE TYPE: protein
 115
 116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 117
 118 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
 119 -20 -15 -10 -5
 120
 121 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 122 1 5 10
 123
 124 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
 125 15 20 25
 126
 127 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
 128 30 35 40
 129
 130 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
 131 45 50 55 60
 132
 133 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
 134 65 70 75
 135
 136 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
 137 80 85 90
 138
 139 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
 140 95 100 105
 141
 142 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
 143 110 115 120
 144
 145 Gly
 146 125
 147
 148 (2) INFORMATION FOR SEQ ID NO:3:
 149
 150 (i) SEQUENCE CHARACTERISTICS:
 151 (A) LENGTH: 461 base pairs
 152 (B) TYPE: nucleic acid

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153 (C) STRANDEDNESS: single
 154 (D) TOPOLOGY: linear
 155
 156 (ii) MOLECULE TYPE: DNA (genomic)
 157
 158
 159 (ix) FEATURE:
 160 (A) NAME/KEY: CDS
 161 (B) LOCATION: 1..459
 162
 163 (ix) FEATURE:
 164 (A) NAME/KEY: mat_peptide
 165 (B) LOCATION: 58
 166
 167
 168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 169
 170 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT 48
 171 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
 172 -19 -15 -10 -5
 173
 174 GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG 96
 175 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 176 1 5 10
 177
 178 TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG 144
 179 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
 180 15 20 25
 181
 182 ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG 192
 183 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
 184 30 35 40 45
 185
 186 GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT 240
 187 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
 188 50 55 60
 189
 190 CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC 288
 191 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
 192 65 70 75
 193
 194 ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC 336
 195 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 196 80 85 90
 197
 198 TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT 384
 199 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
 200 95 100 105
 201
 202 CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC 432
 203 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
 204 110 115 120 125
 205

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461

206 GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
207 Val Tyr Pro Leu Val Pro Gly Ser Leu
208 130

209

210

211 (2) INFORMATION FOR SEQ ID NO:4:

212

213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 153 amino acids
215 (B) TYPE: amino acid
216 (D) TOPOLOGY: linear

217

218 (ii) MOLECULE TYPE: protein

219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

221

222 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
223 -19 -15 -10 -5

224

225 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
226 1 5 10

227

228 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
229 15 20 25

230

231 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
232 30 35 40 45

233

234 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
235 50 55 60

236

237 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
238 65 70 75

239

240 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
241 80 85 90

242

243 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
244 95 100 105

245

246 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
247 110 115 120 125

248

249 Val Tyr Pro Leu Val Pro Gly Ser Leu
250 130

251

252 (2) INFORMATION FOR SEQ ID NO:5:

253

254 (i) SEQUENCE CHARACTERISTICS:
255 (A) LENGTH: 321 base pairs
256 (B) TYPE: nucleic acid
257 (C) STRANDEDNESS: single
258 (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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